



SEQUENCE LISTING

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AUG 28 2003

TECH CENTER 1600/2900

<110> Wu, Hongjian
Crooke, Stanley T.

<120> Human RNase III And Compositions And Uses Thereof

<130> ISIS5029/ISPH-0522

<140> 09/900,425

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<170> PatentIn version 3.1

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          20          25          30

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```

Ser Phe Arg Pro Gln Asn Leu Arg Leu Leu His Pro Gln Gln Pro Pro
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Val Gln Tyr Gln Tyr Glu Pro Pro Ser Ala Pro Ser Thr Thr Phe Ser
50          55          60

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```

Asn Ser Pro Ala Pro Asn Phe Leu Pro Pro Arg Pro Asp Phe Val Pro
65          70          75          80

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Phe Pro Pro Pro Met Pro Pro Ser Ala Gln Gly Pro Leu Pro Pro Cys
          85          90          95

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Pro Ile Arg Pro Pro Phe Pro Asn His Gln Met Arg His Pro Phe Pro
100          105          110

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Val Pro Pro Cys Phe Pro Pro Met Pro Pro Pro Met Pro Cys Pro Asn
115          120          125

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Asn Pro Pro Val Pro Gly Ala Pro Pro Gly Gln Gly Thr Phe Pro Phe
130          135          140

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Met Met Pro Pro Pro Ser Met Pro His Pro Pro Pro Pro Val Met

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Phe	Pro	Pro	Pro	Ser	Phe	Asn	Ser	Phe	Gln	Asn	Asn	Pro	Ser	Ser	Phe
			180					185					190		
Leu	Pro	Ser	Ala	Asn	Asn	Ser	Ser	Ser	Pro	His	Phe	Arg	His	Leu	Pro
		195					200					205			
Pro	Tyr	Pro	Leu	Pro	Lys	Ala	Pro	Ser	Glu	Arg	Arg	Ser	Pro	Glu	Arg
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Leu	Lys	His	Tyr	Asp	Asp	His	Arg	His	Arg	Asp	His	Ser	His	Gly	Arg
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Gly	Glu	Arg	His	Arg	Ser	Leu	Asp	Arg	Arg	Glu	Arg	Gly	Arg	Ser	Pro
				245					250					255	
Asp	Arg	Arg	Arg	Gln	Asp	Ser	Arg	Tyr	Arg	Ser	Asp	Tyr	Asp	Arg	Gly
			260					265					270		
Arg	Thr	Pro	Ser	Arg	His	Arg	Ser	Tyr	Glu	Arg	Ser	Arg	Glu	Arg	Glu
		275					280					285			
Arg	Glu	Arg	His	Arg	His	Arg	Asp	Asn	Arg	Arg	Ser	Pro	Ser	Leu	Glu
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Arg	Ser	Tyr	Lys	Lys	Glu	Tyr	Lys	Arg	Ser	Gly	Arg	Ser	Tyr	Gly	Leu
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Ser	Val	Val	Pro	Glu	Pro	Ala	Gly	Cys	Thr	Pro	Glu	Leu	Pro	Gly	Glu
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Ile	Ile	Lys	Asn	Thr	Asp	Ser	Trp	Ala	Pro	Pro	Leu	Glu	Ile	Val	Asn
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His	Arg	Ser	Pro	Ser	Arg	Glu	Lys	Lys	Arg	Ala	Arg	Trp	Glu	Glu	Glu
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Lys	Asp	Arg	Trp	Ser	Asp	Asn	Gln	Ser	Ser	Gly	Lys	Asp	Lys	Asn	Tyr
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Thr Ser Ile Lys Glu Lys Glu Pro Glu Glu Thr Met Pro Asp Lys Asn
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Glu Glu Glu Glu Glu Glu Leu Leu Lys Pro Val Trp Ile Arg Cys Thr
 405 410 415

His Ser Glu Asn Tyr Tyr Ser Ser Asp Pro Met Asp Gln Val Gly Asp
 420 425 430

Ser Thr Val Val Gly Thr Ser Arg Leu Arg Asp Leu Tyr Asp Lys Phe
 435 440 445

Glu Glu Glu Leu Gly Ser Arg Gln Glu Lys Ala Lys Ala Ala Arg Pro
 450 455 460

Pro Trp Glu Pro Pro Lys Thr Lys Leu Asp Glu Asp Leu Glu Ser Ser
 465 470 475 480

Ser Glu Ser Glu Cys Glu Ser Asp Glu Asp Ser Thr Cys Ser Ser Ser
 485 490 495

Ser Asp Ser Glu Val Phe Asp Val Ile Ala Glu Ile Lys Arg Lys Lys
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Ala His Pro Asp Arg Leu His Asp Glu Leu Trp Tyr Asn Asp Pro Gly
 515 520 525

Gln Met Asn Asp Gly Pro Leu Cys Lys Cys Ser Ala Lys Ala Arg Arg
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Thr Gly Ile Arg His Ser Ile Tyr Pro Gly Glu Glu Ala Ile Lys Pro
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Cys Arg Pro Met Thr Asn Asn Ala Gly Arg Leu Phe His Tyr Arg Ile
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Thr Val Ser Pro Pro Thr Asn Phe Leu Thr Asp Arg Pro Thr Val Ile
 580 585 590

Glu Tyr Asp Asp His Glu Tyr Ile Phe Glu Gly Phe Ser Met Phe Ala
 595 600 605

His Ala Pro Leu Thr Asn Ile Pro Leu Cys Lys Val Ile Arg Phe Asn
610 615 620

Ile Asp Tyr Thr Ile His Phe Ile Glu Glu Met Met Pro Glu Asn Phe
625 630 635 640

Cys Val Lys Gly Leu Glu Leu Phe Ser Leu Phe Leu Phe Arg Asp Ile
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660 665 670

Pro Pro Cys Cys Pro Arg Phe His Phe Met Pro Arg Phe Val Arg Phe
675 680 685

Leu Pro Asp Gly Gly Lys Glu Val Leu Ser Met His Gln Ile Leu Leu
690 695 700

Tyr Leu Leu Arg Cys Ser Lys Ala Leu Val Pro Glu Glu Glu Ile Ala
705 710 715 720

Asn Met Leu Gln Trp Glu Glu Leu Glu Trp Gln Lys Tyr Ala Glu Glu
725 730 735

Cys Lys Gly Met Ile Val Thr Asn Pro Gly Thr Lys Pro Ser Ser Val
740 745 750

Arg Ile Asp Gln Leu Asp Arg Glu Gln Phe Asn Pro Asp Val Ile Thr
755 760 765

Phe Pro Ile Ile Val His Phe Gly Ile Arg Pro Ala Gln Leu Ser Tyr
770 775 780

Ala Gly Asp Pro Gln Tyr Gln Lys Leu Trp Lys Ser Tyr Val Lys Leu
785 790 795 800

Arg His Leu Leu Ala Asn Ser Pro Lys Val Lys Gln Thr Asp Lys Gln
805 810 815

Lys Leu Ala Gln Arg Glu Glu Ala Leu Gln Lys Ile Arg Gln Lys Asn
820 825 830

Thr Met Arg Arg Glu Val Thr Val Glu Leu Ser Ser Gln Gly Phe Trp
835 840 845

Lys Thr Gly Ile Arg Ser Asp Val Cys Gln His Ala Met Met Leu Pro
850 855 860

Val Leu Thr His His Ile Arg Tyr His Gln Cys Leu Met His Leu Asp
865 870 875 880

Lys Leu Ile Gly Tyr Thr Phe Gln Asp Arg Cys Leu Leu Gln Leu Ala
885 890 895

Met Thr His Pro Ser His His Leu Asn Phe Gly Met Asn Pro Asp His
900 905 910

Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln Pro Lys Tyr Gly
915 920 925

Asp Arg Lys Val His His Met His Met Arg Lys Lys Gly Ile Asn Thr
930 935 940

Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp Pro Thr Pro Ser
945 950 955 960

Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Val
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Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe Pro Ser Leu Glu
980 985 990

Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val Gln Asn Gln His
995 1000 1005

Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro Phe Met Leu Tyr
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Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu Arg His Ala Met
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Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr Ser Pro Val Leu 1090 1095 1100		
Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val Ile Phe Thr His 1105 1110 1115 1120		
Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr Val Gly Phe Asn 1125 1130 1135		
His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe Leu Gly Asp Ser 1140 1145 1150		
Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile His Phe Pro Asp 1155 1160 1165		
His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser Leu Val Asn Asn 1170 1175 1180		
Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met Gln Glu Tyr Ala 1185 1190 1195 1200		
Ile Thr Asn Asp Lys Thr Lys Arg Pro Val Gly Leu Arg Thr Lys Thr 1205 1210 1215		
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Asp Leu Glu Tyr Val His Thr Phe Met Asn Val Cys Phe Phe Pro Arg 1235 1240 1245		
Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Asp Pro Lys Ser Gln 1250 1255 1260		
Leu Gln Gln Cys Cys Leu Thr Leu Arg Thr Glu Gly Lys Glu Pro Asp 1265 1270 1275 1280		
Ile Pro Leu Tyr Lys Thr Leu Gln Thr Val Gly Pro Ser His Ala Arg 1285 1290 1295		

Thr Tyr Thr Val Ala Val Tyr Phe Lys Gly Glu Arg Ile Gly Cys Gly
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Lys Gly Pro Ser Ile Gln Gln Ala Glu Met Gly Ala Ala Met Asp Ala
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Leu Glu Lys Tyr Asn Phe Pro Gln Met Ala His Gln Lys Arg Phe Ile
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Gly Arg Lys Tyr Arg Gln Glu Leu Lys Glu Met Arg Trp Glu Arg Glu
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35 40 45

Gly Leu Ala Thr Tyr Arg Thr Ala Leu Val Gln Asn Arg Asn Leu Ala
50 55 60

Thr Leu Ala Lys Asn Cys Arg Ile Asp Glu Met Leu Gln Tyr Ser His
65 70 75 80

Gly Ala Asp Leu Ile Asn Val Ala Glu Phe Lys His Ala Leu Ala Asn
85 90 95

Ala Phe Glu Ala Val Met Ala Ala Ile Tyr Leu Asp Gly Gly Leu Ala
100 105 110

Pro Cys Asp Val Ile Phe Ser Lys Ala Met Tyr Gly His Gln Pro Val
 115 120 125

Leu Lys Glu Lys Trp Asp His Ile Asn Glu His Glu Leu Lys Arg Glu
 130 135 140

Asp Pro Gln Gly Asp Arg Asp Leu Ser Phe Ile Thr Pro Thr Leu Ser
 145 150 155 160

Thr Phe His Ala Leu Glu Glu Arg Leu Gly Ile Gln Phe Asn Asn Ile
 165 170 175

Arg Leu Leu Ala Lys Ala Phe Thr Arg Arg Asn Ile Pro Asn Asn Asp
 180 185 190

Leu Thr Lys Gly His Asn Gln Arg Leu Glu Trp Leu Gly Asp Ser Val
 195 200 205

Leu Gln Leu Ile Val Ser Asp Phe Leu Tyr Arg Arg Phe Pro Tyr His
 210 215 220

His Glu Gly His Met Ser Leu Leu Arg Thr Ser Leu Val Ser Asn Gln
 225 230 235 240

Thr Gln Ala Val Val Cys Asp Asp Leu Gly Phe Thr Glu Phe Val Ile
 245 250 255

Lys Ala Pro Tyr Lys Thr Pro Glu Leu Lys Leu Lys Asp Lys Ala Asp
 260 265 270

Leu Val Glu Ala Phe Ile Gly Ala Leu Tyr Val Asp Arg Gly Ile Glu
 275 280 285

His Cys Arg Ala Phe Ile Arg Ile Val Phe Cys Pro Arg Leu Lys His
 290 295 300

Phe Ile Glu Ser Glu Lys Trp Asn Asp Ala Lys Ser His Leu Gln Gln
 305 310 315 320

Trp Cys Leu Ala Met Arg Asp Pro Ser Ser Ser Glu Pro Asp Met Pro
 325 330 335

Glu Tyr Arg Val Leu Gly Ile Glu Gly Pro Thr Asn Asn Arg Ile Phe
 340 345 350

Lys Ile Ala Val Tyr Tyr Lys Gly Lys Arg Leu Ala Ser Ala Ala Glu
 355 360 365

Ser Asn Val His Lys Ala Glu Leu Arg Val Ala Glu Leu Ala Leu Ala
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Asn Leu Glu Ser Met Ser Phe Ser Lys Met Lys Ala Lys Asn Asn Ser
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Asn Met Arg Arg Arg Leu Glu Gln Asp Thr Ser Asp
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Arg Ser Ser His Ile Lys Asn Arg Gln Tyr Tyr Ile Leu Glu Lys Lys
 35 40 45

Ile Arg Lys Leu Met Phe Ala Met Lys Ala Leu Leu Glu Glu Thr Lys
 50 55 60

His Ser Thr Lys Asp Asp Val Asn Leu Val Ile Pro Gly Ser Thr Trp
 65 70 75 80

Ser His Ile Glu Gly Val Tyr Glu Met Leu Lys Ser Arg His Asp Arg
 85 90 95

Gln Asn Glu Pro Val Ile Glu Glu Pro Ser Ser His Pro Lys Asn Gln
 100 105 110

Lys Asn Gln Glu Asn Asn Glu Pro Thr Ser Glu Glu Phe Glu Glu Gly
 115 120 125

Glu Tyr Pro Pro Pro Leu Pro Pro Leu Arg Ser Glu Lys Leu Lys Glu
 130 135 140

Gln Val Phe Met His Ile Ser Arg Ala Tyr Glu Ile Tyr Pro Asn Gln
 145 150 155 160

Ser Asn Pro Asn Glu Leu Leu Asp Ile His Asn Glu Arg Leu Glu Phe
 165 170 175

Leu Gly Asp Ser Phe Phe Asn Leu Phe Thr Thr Arg Ile Ile Phe Ser
 180 185 190

Lys Phe Pro Gln Met Asp Glu Gly Ser Leu Ser Lys Leu Arg Ala Lys
 195 200 205

Phe Val Gly Asn Glu Ser Ala Asp Lys Phe Ala Arg Leu Tyr Gly Phe
 210 215 220

Asp Lys Thr Leu Val Leu Ser Tyr Ser Ala Glu Lys Asp Gln Leu Arg
 225 230 235 240

Lys Ser Gln Lys Val Ile Ala Asp Thr Phe Glu Ala Tyr Leu Gly Ala
 245 250 255

Leu Ile Leu Asp Gly Gln Glu Glu Thr Ala Phe Gln Trp Val Ser Arg
 260 265 270

Leu Leu Gln Pro Lys Ile Ala Asn Ile Thr Val Gln Arg Pro Ile Asp
 275 280 285

Lys Leu Ala Lys Ser Lys Leu Phe His Lys Tyr Ser Thr Leu Gly His
 290 295 300

Ile Glu Tyr Arg Trp Pro Ala Cys Val Asp Gly Ala Gly Gly Ser Ala
 305 310 315 320

Glu Gly Tyr Val Ile Ala Cys Ile Phe Asn Gly Lys Glu Val Ala Arg
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 35 40 45

Val Ile Gln Leu Glu His Ala Val Thr Lys Leu Val Glu Ser Tyr Asn
 50 55 60

Lys Ile Ile Glu Leu Ser Pro Asn Leu Val Ala Tyr Asn Glu Ala Val
 65 70 75 80

Asn Asn Gln Asp Arg Val Pro Val Gln Ile Leu Pro Ser Leu Ser Arg
 85 90 95

Tyr Gln Leu Lys Leu Ala Ala Glu Leu Lys Thr Leu His Asp Leu Lys
 100 105 110

Lys Asp Ala Ile Leu Thr Glu Ile Thr Asp Tyr Glu Asn Glu Phe Asp
 115 120 125

Thr Glu Gln Lys Gln Pro Ile Leu Gln Glu Ile Ser Lys Ala Asp Met
 130 135 140

Glu Lys Leu Glu Lys Leu Glu Gln Val Lys Arg Glu Lys Arg Glu Lys
 145 150 155 160

Ile Asp Val Asn Val Tyr Glu Asn Leu Asn Glu Lys Glu Asp Glu Glu
 165 170 175

Glu Asp Glu Gly Glu Asp Ser Tyr Asp Pro Thr Lys Ala Gly Asp Ile
 180 185 190

Val Lys Ala Thr Lys Trp Pro Pro Lys Leu Pro Glu Ile Gln Asp Leu
 195 200 205

Ala Ile Arg Ala Arg Val Phe Ile His Lys Ser Thr Ile Lys Asp Lys
210 215 220

Val Tyr Leu Ser Gly Ser Glu Met Ile Asn Ala His Asn Glu Arg Leu
225 230 235 240

Glu Phe Leu Gly Asp Ser Ile Leu Asn Ser Val Met Thr Leu Ile Ile
245 250 255

Tyr Asn Lys Phe Pro Asp Tyr Ser Glu Gly Gln Leu Ser Thr Leu Arg
260 265 270

Met Asn Leu Val Ser Asn Glu Gln Ile Lys Gln Trp Ser Ile Met Tyr
275 280 285

Asn Phe His Glu Lys Leu Lys Thr Asn Phe Asp Leu Lys Asp Glu Asn
290 295 300

Ser Asn Phe Gln Asn Gly Lys Leu Lys Leu Tyr Ala Asp Val Phe Glu
305 310 315 320

Ala Tyr Ile Gly Gly Leu Met Glu Asp Asp Pro Arg Asn Asn Leu Pro
325 330 335

Lys Ile Arg Lys Trp Leu Arg Lys Leu Ala Lys Pro Val Ile Glu Glu
340 345 350

Ala Thr Arg Asn Gln Val Ala Leu Glu Lys Thr Asp Lys Leu Asp Met
355 360 365

Asn Ala Lys Arg Gln Leu Tyr Ser Leu Ile Gly Tyr Ala Ser Leu Arg
370 375 380

Leu His Tyr Val Thr Val Lys Lys Pro Thr Ala Val Asp Pro Asn Ser
385 390 395 400

Ile Val Glu Cys Arg Val Gly Asp Gly Thr Val Leu Gly Thr Gly Val
405 410 415

Gly Arg Asn Ile Lys Ile Ala Gly Ile Arg Ala Ala Glu Asn Ala Leu
420 425 430

Arg Asp Lys Lys Met Leu Asp Phe Tyr Ala Lys Gln Arg Ala Ala Ile
 435 440 445

Pro Arg Ser Glu Ser Val Leu Lys Asp Pro Ser Gln Lys Asn Lys Lys
 450 455 460

Arg Lys Phe Ser Asp Thr Ser
 465 470

<210> 6
 <211> 226
 <212> PRT
 <213> Escherichia coli

<400> 6

Met Asn Pro Ile Val Ile Asn Arg Leu Gln Arg Lys Leu Gly Tyr Thr
 1 5 10 15

Phe Asn His Gln Glu Leu Leu Gln Gln Ala Leu Thr His Arg Ser Ala
 20 25 30

Ser Ser Lys His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser Ile Leu
 35 40 45

Ser Tyr Val Ile Ala Asn Ala Leu Tyr His Arg Phe Pro Arg Val Asp
 50 55 60

Glu Gly Asp Met Ser Arg Met Arg Ala Thr Leu Val Arg Gly Asn Thr
 65 70 75 80

Leu Ala Glu Leu Ala Arg Glu Phe Glu Leu Gly Glu Cys Leu Arg Leu
 85 90 95

Gly Pro Gly Glu Leu Lys Ser Gly Gly Phe Arg Arg Glu Ser Ile Leu
 100 105 110

Ala Asp Thr Val Glu Ala Leu Ile Gly Gly Val Phe Leu Asp Ser Asp
 115 120 125

Ile Gln Thr Val Glu Lys Leu Ile Leu Asn Trp Tyr Gln Thr Arg Leu
 130 135 140

Asp Glu Ile Ser Pro Gly Asp Lys Gln Lys Asp Pro Lys Thr Arg Leu

145 150 155 160

Gln Glu Tyr Leu Gln Gly Arg His Leu Pro Leu Pro Thr Tyr Leu Val
165 170 175

Val Gln Val Arg Gly Glu Ala His Asp Gln Glu Phe Thr Ile His Cys
180 185 190

Gln Val Ser Gly Leu Ser Glu Pro Val Val Gly Thr Gly Ser Ser Arg
195 200 205

Arg Lys Ala Glu Gln Ala Ala Ala Glu Gln Ala Leu Lys Lys Leu Glu
210 215 220

Leu Glu
225

<210> 7
<211> 11
<212> PRT
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<400> 7

His Asn Glu Arg Leu Glu Phe Leu Gly Asp Ser
1 5 10

<210> 8
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<400> 8
atccctttct tccgcatgtg 20

<210> 9
<211> 20
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<223> Synthetic

<400> 9
gccaaaggcgt gacatgatat 20

<210> 10

<211> 20
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<213> Artificial Sequence
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<223> Synthetic

<400> 10
cggatcatta aagagcaagc 20

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence
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<223> Synthetic

<400> 11
tattcaccaa agagcttcgc 20

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence
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<223> Synthetic

<400> 12
caatcgtgga aagaagcaga 20

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence
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<223> Synthetic

<400> 13
gctcccatTT cgccttgctg 20

<210> 14
<211> 20
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<223> Synthetic

<400> 14
atgctctctt tcccaccta 20

<210> 15
<211> 20
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<213> Artificial Sequence
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<223> Synthetic

<400> 15
aaatactcca cacttgcatg 20

<210> 16
<211> 20
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<213> Artificial Sequence
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<223> Synthetic

<400> 16
tgcacattca ccaaagtcaa 20

<210> 17
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<400> 17
agtctagggt cacaatctgg 20

<210> 18
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<213> Artificial Sequence
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<400> 18
ttcagttgta gtgggccgac 20

<210> 19
<211> 40
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<213> Artificial Sequence
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<223> Synthetic

<400> 19
caaggcacgc ctctcagatc gctagagaag gcttttctca 40

<210> 20
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<213> Artificial Sequence
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<223> Synthetic

<400> 20

cattaattct cgcagctagc gctgcgttct tcatcgacgc

40

<210> 21

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

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ccaaatactg atcgacaact tattgaaaact tctcc

35

<210> 22

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 22

gagtttgaag aagcaattgg agtaattttt actcatg

37

<210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 23

tcgacttctg gcaagggcat tcacatt

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<210> 24

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 24

cctctgtgcc agcttctggt tgtcag

26

<210> 25

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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<210> 26	
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tttgctagga ggtggcgaag tttcac	26
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aatgctgtgc ctaattcctg tgcgtcttgc	30
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cagggtgctgt cctcatcaga ctcacactcg gattcactgg aactctct	48
<210> 30	
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cactgggcag gaaagaacta gggttg	26

<210> 31
 <211> 26
 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic

<400> 31
 tggaaactat taaaactggg aggtgg

26

<210> 32
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 <212> DNA
 <213> Artificial Sequence
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<400> 32
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50

<210> 33
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 <212> DNA
 <213> Artificial Sequence
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<400> 33
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40

<210> 34
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 <212> DNA
 <213> Artificial Sequence
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 <223> Synthetic

<400> 34
 cattaattct cgcagctagc gctgcgttct tcatcgacgc

40

<210> 35
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 <212> PRT
 <213> Homo sapiens
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Cys Arg Ser Asp Tyr Asp Arg Gly Arg Thr Pro Ser Arg His Arg Ser
 1 5 10 15

Tyr Glu Arg Ser

20

<210> 36
<211> 20
<212> PRT
<213> Homo sapiens
<400> 36

Cys Arg Trp Glu Arg Glu His Gln Glu Arg Glu Pro Asp Glu Thr Glu
1 5 10 15

Asp Ile Lys Lys
20

<210> 37
<211> 466
<212> PRT
<213> Homo sapiens

<400> 37

Asn Pro Asp His Ala Arg Asn Ser Leu Ser Asn Cys Gly Ile Arg Gln
1 5 10 15

Pro Lys Tyr Gly Asp Arg Lys Val His His Met His Met Arg Lys Lys
20 25 30

Gly Ile Asn Thr Leu Ile Asn Ile Met Ser Arg Leu Gly Gln Asp Asp
35 40 45

Pro Thr Pro Ser Arg Ile Asn His Asn Glu Arg Leu Glu Phe Leu Gly
50 55 60

Asp Ala Val Val Glu Phe Leu Thr Ser Val His Leu Tyr Tyr Leu Phe
65 70 75 80

Pro Ser Leu Glu Glu Gly Gly Leu Ala Thr Tyr Arg Thr Ala Ile Val
85 90 95

Gln Asn Gln His Leu Ala Met Leu Ala Lys Lys Leu Glu Leu Asp Pro
100 105 110

Phe Met Leu Tyr Ala His Gly Pro Asp Leu Cys Arg Glu Ser Asp Leu
115 120 125

Arg His Ala Met Ala Asn Cys Phe Glu Ala Leu Ile Gly Ala Val Tyr
130 135 140

Leu Glu Gly Ser Leu Glu Glu Ala Lys Gln Leu Phe Gly Arg Leu Leu
 145 150 155 160

Phe Asn Asp Pro Asp Leu Arg Glu Val Trp Leu Asn Tyr Pro Leu His
 165 170 175

Pro Leu Gln Leu Gln Glu Pro Asn Thr Asp Arg Gln Leu Ile Glu Thr
 180 185 190

Ser Pro Val Leu Gln Lys Leu Thr Glu Phe Glu Glu Ala Ile Gly Val
 195 200 205

Ile Phe Thr His Val Arg Leu Leu Ala Arg Ala Phe Thr Leu Arg Thr
 210 215 220

Val Gly Phe Asn His Leu Thr Leu Gly His Asn Gln Arg Met Glu Phe
 225 230 235 240

Leu Gly Asp Ser Ile Met Gln Leu Val Ala Thr Glu Tyr Leu Phe Ile
 245 250 255

His Phe Pro Asp His His Glu Gly His Leu Thr Leu Leu Arg Ser Ser
 260 265 270

Leu Val Asn Asn Arg Thr Gln Ala Lys Val Ala Glu Glu Leu Gly Met
 275 280 285

Gln Glu Tyr Ala Ile Thr Asn Asp Lys Thr Lys Arg Pro Val Gly Leu
 290 295 300

Arg Thr Lys Thr Leu Ala Asp Leu Leu Glu Ser Phe Ile Ala Ala Leu
 305 310 315 320

Tyr Thr Asp Lys Asp Leu Glu Tyr Val His Thr Phe Met Asn Val Cys
 325 330 335

Phe Phe Pro Arg Leu Lys Glu Phe Ile Leu Asn Gln Asp Trp Asn Asp
 340 345 350

Pro Lys Ser Gln Leu Gln Gln Cys Cys Leu Thr Leu Arg Thr Glu Gly
 355 360 365

Lys Glu Pro Asp Ile Pro Leu Tyr Lys Thr Leu Gln Thr Val Gly Pro
370 375 380

Ser His Ala Arg Thr Tyr Thr Val Ala Val Tyr Phe Lys Gly Glu Arg
385 390 395 400

Ile Gly Cys Gly Lys Gly Pro Ser Ile Gln Gln Ala Glu Met Gly Ala
405 410 415

Ala Met Asp Ala Leu Glu Lys Tyr Asn Phe Pro Gln Met Ala His Gln
420 425 430

Lys Arg Phe Ile Gly Arg Lys Tyr Arg Gln Glu Leu Lys Glu Met Arg
435 440 445

Trp Glu Arg Glu His Gln Glu Arg Glu Pro Asp Glu Thr Glu Asp Ile
450 455 460

Lys Lys
465